

SEQUENCE LISTING

<110> Ajinomoto Co. Inc.

<120>

<130> OP1628

<150> JP 2002-336340

<151> 2002-11-20

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

agggaattcc ccgttctgga taatgtttt tgcggcgac

39

<210> 2

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

cggatgcac tagagttaac ctgcagggtg aaattgttat ccgctcacaa ttccacac 58

<210> 3

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

tgacctgcag gtttgcacag aggatggccc atgtt 35

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 4
cattctagat ccctaaactt tacagcaaac cggcat 36

<210> 5
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 5
catttcctgc aggcaaagga gatgagcgta atggtgatca tggaaatctt cattacaggt 60
ctgc 64

<210> 6
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6
gggcgagcta gaagagctcc aaaacccgcg aaaactaacc catcaacatc 50

<210> 7
<211> 711
<212> DNA
<213> Brevibacterium lactofermentum

<220>
<221> CDS
<222> (1)..(711)

<400> 7

atg	gtg	atc	atg	gaa	atc	ttc	att	aca	ggt	ctg	ctt	ttg	ggg	gcc	agt	48	
Met	Val	Ile	Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser		
1	5	10	15														
ctt	tta	ctg	tcc	atc	gga	ccg	cag	aat	gta	ctg	gtg	att	aaa	caa	gga	96	
Leu	Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
20	25	30															
att	aag	cgc	gaa	gga	ctc	att	gcg	gtt	ctt	ctc	gtg	tgt	tta	att	tct	144	
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser		
35	40	45															
gac	gtc	ttt	ttg	ttc	atc	gcc	ggc	acc	ttg	ggc	gtt	gat	ctt	ttg	tcc	192	
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser		
50	55	60															
aat	gcc	gcg	ccg	atc	gtg	ctc	gat	att	atg	cgc	tgg	ggt	ggc	atc	gct	240	
Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala		
65	70	75	80														
tac	ctg	tta	tgg	ttt	gcc	gtc	atg	gca	gcg	aaa	gac	gcc	atg	aca	aac	288	
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn		
85	90	95															
aag	gtg	gaa	gcg	cca	cag	atc	att	gaa	gaa	aca	gaa	cca	acc	gtg	ccc	336	
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro		
100	105	110															
gat	gac	acg	cct	ttg	ggc	ggt	tcg	gcg	gtg	gcc	act	gac	acg	cgc	aac	384	
Asp	Asp	Thr	Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn		
115	120	125															
cgg	gtg	cgg	gtg	gag	gtg	agc	gtc	gat	aag	cag	cg	gtt	tgg	gta	aag	432	
Arg	Val	Arg	Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys		
130	135	140															
ccc	atg	ttg	atg	gca	atc	gtg	ctg	acc	tgg	ttg	aac	ccg	aat	gcg	tat	480	
Pro	Met	Leu	Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr		
145	150	155	160														
ttg	gac	gcg	ttt	gtg	ttt	atc	ggc	ggc	gtc	ggc	g	caa	tac	ggc	gac	528	
Leu	Asp	Ala	Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp		
165	170	175															
acc	gga	cgg	tgg	att	ttc	gcc	gct	ggc	g	tc	g	ca	agc	ctg	atc	576	
Thr	Gly	Arg	Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile		
180	185	190															
tgg	ttc	ccg	ctg	gtg	ggt	ttc	ggc	gca	gca	gca	ttg	tca	cgc	ccg	ctg	624	
Trp	Phe	Pro	Leu	Val	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu				
195	200	205															
tcc	agc	ccc	aag	gtg	tgg	cgc	tgg	atc	aac	gtc	gtc	gtg	gca	gtt	gtg	672	
Ser	Ser	Pro	Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val		
210	215	220															
atg	acc	gca	ttg	gcc	atc	aaa	ctg	atg	ttg	atg	ggt	tag			711		
Met	Thr	Ala	Leu	Ala	Ile	Lys	Leu	Met	Leu	Met	Gly						

225

230

235

<210> 8

<211> 236

<212> PRT

<213> *Brevibacterium lactofermentum*

<400> 8

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser
1 5 10 15
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
20 25 30
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
35 40 45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
100 105 110
Asp Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn
115 120 125
Arg Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys
130 135 140
Pro Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr
145 150 155 160
Leu Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp
165 170 175
Thr Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile
180 185 190
Trp Phe Pro Leu Val Gly Phe Gly Ala Ala Leu Ser Arg Pro Leu
195 200 205
Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val
210 215 220
Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
225 230 235

<210> 9

<211> 712

<212> DNA

<213> *Brevibacterium lactofermentum*

<220>

<221> CDS

<222> (1).. (375)

<400> 9

atg	gtg	atc	atg	gaa	atc	ttc	att	aca	ggt	ctg	ctt	ttg	ggg	gcc	agt	48
Met	Val	Ile	Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser	
1			5					10						15		
ctt	ttg	ctg	tcc	atc	gga	ccg	cag	aat	gta	ctg	gtg	att	aaa	caa	gga	96
Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
			20					25						30		
att	aag	cgc	gaa	gga	ctc	att	gcg	gtt	ctt	ctc	gtg	tgt	tta	att	tct	144
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser	
			35				40					45				
gac	gtc	ttt	ttg	ttc	atc	gcc	ggc	acc	ttg	ggc	gtt	gat	ctt	ttg	tcc	192
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser	
			50			55					60					
aat	gcc	gcg	ccg	atc	gtg	ctc	gat	att	atg	cgc	tgg	ggt	ggc	atc	gct	240
Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala	
			65			70			75			80				
tac	ctg	tta	tgg	ttt	gcc	gtc	atg	gca	gcg	aaa	gac	gcc	atg	aca	aac	288
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	
			85					90					95			
aag	gtg	gaa	gcg	cca	cag	atc	att	gaa	gaa	aca	gaa	cca	acc	gtg	ccc	336
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro	
			100			105						110				
gat	gac	acg	cct	ttg	ggc	gtg	ttc	ggc	ggt	ggc	cac	tga	cacgcgcac		385	
Asp	Asp	Thr	Pro	Leu	Gly	Val	Phe	Gly	Gly	Gly	His					
			115			120						125				
cgggtgcggg	tggaggtgag	cgtcgataag	cagcgggttt	gggtgaagcc	catgttgatg											445
gcaatcgatgc	tgacactgggtt	gaacccgaat	gcgtattttgg	acgcgtttgt	gtttatcgac											505
ggcgatcgatgc	cgcaatacgg	cgacaccgga	cggtggattt	tcgcccgtgg	cgcgttcgcg											565
gcaaggctgtatgc	tctgggtccc	gctgggtgggt	ttcggcgcag	cagcattgtc	acgcccgtg											625
tccagccccca	agggtgtggcg	ctggatcaac	gtcgtcgatgg	cagttgtgat	gaccgcattg											685
gccatcaaac	tgtatgttgc	gggttag														712

<210> 10

<211> 124

<212> PRT

<213> Brevibacterium lactofermentum

<400> 10

Met	Val	Ile	Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser	
1			5					10					15			
Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
			20			25						30				

Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
35 40 45
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
50 55 60
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
65 70 75 80
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
85 90 95
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
100 105 110
Asp Asp Thr Pro Leu Gly Val Phe Gly Gly His
115 120

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

aaagaattcg cacggatcac tgtattcggc tgcaacttt

39

<210> 12

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

aaagaattcg ccgtgttgct aggatggttg ttcttggtac a

41

<210> 13

<211> 1197

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (272)..(1153)

<400> 13

ccaggcgact gtcttcaata ttacagccgc aactactgac atgacgggtg atgggttca 60
caattccacg gcgatcgca cccaaacgcag tgcacccag ataatgtgtt gcgatgacag 120
tgtcaaactg gttattcctt taaggggtga gttttctta agggaaagcat aaaaaaaaaaca 180
tgcataacaac aatcagaacg gttctgtctg cttgccttta atgccttacc aaacgttacca 240
ttgagacact tgttgcaca gaggatggcc c atg ttc acg gga agt att gtc 292
Met Phe Thr Gly Ser Ile Val
1 5
gcg att gtt act ccg atg gat gaa aaa ggt aat gtc tgt cgg gct agc 340
Ala Ile Val Thr Pro Met Asp Glu Lys Gly Asn Val Cys Arg Ala Ser
10 15 20
ttg aaa aaa ctg att gat tat cat gtc gcc agc ggt act tcg gcg atc 388
Leu Lys Lys Leu Ile Asp Tyr His Val Ala Ser Gly Thr Ser Ala Ile
25 30 35
gtt tct gtt ggc acc act ggc gag tcc gct acc tta aat cat gac gaa 436
Val Ser Val Gly Thr Thr Gly Glu Ser Ala Thr Leu Asn His Asp Glu
40 45 50 55
cat gct gat gtg gtg atg atg acg ctg gat ctg gct gat ggg cgc att 484
His Ala Asp Val Val Met Met Thr Leu Asp Leu Ala Asp Gly Arg Ile
60 65 70
ccg gta att gcc ggg acc ggc gct aac gct act gcg gaa gcc att agc 532
Pro Val Ile Ala Gly Thr Gly Ala Asn Ala Thr Ala Glu Ala Ile Ser
75 80 85
ctg acg cag cgc ttc aat gac agt ggt atc gtc ggc tgc ctg acg gta 580
Leu Thr Gln Arg Phe Asn Asp Ser Gly Ile Val Gly Cys Leu Thr Val
90 95 100
acc cct tac tac aat cgt ccg tcg caa gaa ggt ttg tat cag cat ttc 628
Thr Pro Tyr Tyr Asn Arg Pro Ser Gln Glu Gly Leu Tyr Gln His Phe
105 110 115
aaa gcc atc gct gag cat act gac ctg ccg caa att ctg tat aat gtg 676
Lys Ala Ile Ala Glu His Thr Asp Leu Pro Gln Ile Leu Tyr Asn Val
120 125 130 135
ccg tcc cgt act ggc tgc gat ctg ctc ccg gaa acg gtg ggc cgt ctg 724
Pro Ser Arg Thr Gly Cys Asp Leu Leu Pro Glu Thr Val Gly Arg Leu
140 145 150
gcg aaa gta aaa aat att atc gga atc aaa gag gca aca ggg aac tta 772
Ala Lys Val Lys Asn Ile Ile Gly Ile Lys Glu Ala Thr Gly Asn Leu
155 160 165
acg cgt gta aac cag atc aaa gag ctg gtt tca gat gat ttt gtt ctg 820
Thr Arg Val Asn Gln Ile Lys Glu Leu Val Ser Asp Asp Phe Val Leu
170 175 180
ctg agc ggc gat gat gcg agc gcg ctg gac ttc atg caa ttg ggc ggt 868
Leu Ser Gly Asp Asp Ala Ser Ala Leu Asp Phe Met Gln Leu Gly Gly
185 190 195

cat ggg gtt att tcc gtt acg act aac gtc gca gcg cgt gat atg gcc	916
His Gly Val Ile Ser Val Thr Thr Asn Val Ala Ala Arg Asp Met Ala	
200 205 210 215	
cag atg tgc aaa ctg gca gca gaa gaa cat ttt gcc gag gca cgc gtt	964
Gln Met Cys Lys Leu Ala Ala Glu Glu His Phe Ala Glu Ala Arg Val	
220 225 230	
att aat cag cgt ctg atg cca tta cac aac aaa cta ttt gtc gaa ccc	1012
Ile Asn Gln Arg Leu Met Pro Leu His Asn Lys Leu Phe Val Glu Pro	
235 240 245	
aat cca atc ccg gtg aaa tgg gca tgt aag gaa ctg ggt ctt gtg gcg	1060
Asn Pro Ile Pro Val Lys Trp Ala Cys Lys Glu Leu Gly Leu Val Ala	
250 255 260	
acc gat acg ctg cgc ctg cca atg aca cca atc acc gac agt ggt cgt	1108
Thr Asp Thr Leu Arg Leu Pro Met Thr Pro Ile Thr Asp Ser Gly Arg	
265 270 275	
gag acg gtc aga gcg gcg ctt aag cat gcc ggt ttg ctg taa	1150
Glu Thr Val Arg Ala Ala Leu Lys His Ala Gly Leu Leu	
280 285 290	
agtttaggga gattttaggg cttactctgt tcaaaagtcg cgcctgg	1197

<210> 14
 <211> 292
 <212> PRT
 <213> Escherichia coli

<400> 14	
Met Phe Thr Gly Ser Ile Val Ala Ile Val Thr Pro Met Asp Glu Lys	
1 5 10 15	
Gly Asn Val Cys Arg Ala Ser Leu Lys Lys Leu Ile Asp Tyr His Val	
20 25 30	
Ala Ser Gly Thr Ser Ala Ile Val Ser Val Gly Thr Thr Gly Glu Ser	
35 40 45	
Ala Thr Leu Asn His Asp Glu His Ala Asp Val Val Met Met Thr Leu	
50 55 60	
Asp Leu Ala Asp Gly Arg Ile Pro Val Ile Ala Gly Thr Gly Ala Asn	
65 70 75 80	
Ala Thr Ala Glu Ala Ile Ser Leu Thr Gln Arg Phe Asn Asp Ser Gly	
85 90 95	
Ile Val Gly Cys Leu Thr Val Thr Pro Tyr Tyr Asn Arg Pro Ser Gln	
100 105 110	
Glu Gly Leu Tyr Gln His Phe Lys Ala Ile Ala Glu His Thr Asp Leu	
115 120 125	
Pro Gln Ile Leu Tyr Asn Val Pro Ser Arg Thr Gly Cys Asp Leu Leu	
130 135 140	
Pro Glu Thr Val Gly Arg Leu Ala Lys Val Lys Asn Ile Ile Gly Ile	

145 150 155 160
Lys Glu Ala Thr Gly Asn Leu Thr Arg Val Asn Gln Ile Lys Glu Leu
165 170 175
Val Ser Asp Asp Phe Val Leu Leu Ser Gly Asp Asp Ala Ser Ala Leu
180 185 190
Asp Phe Met Gln Leu Gly Gly His Gly Val Ile Ser Val Thr Thr Asn
195 200 205
Val Ala Ala Arg Asp Met Ala Gln Met Cys Lys Leu Ala Ala Glu Glu
210 215 220
His Phe Ala Glu Ala Arg Val Ile Asn Gln Arg Leu Met Pro Leu His
225 230 235 240
Asn Lys Leu Phe Val Glu Pro Asn Pro Ile Pro Val Lys Trp Ala Cys
245 250 255
Lys Glu Leu Gly Leu Val Ala Thr Asp Thr Leu Arg Leu Pro Met Thr
260 265 270
Pro Ile Thr Asp Ser Gly Arg Glu Thr Val Arg Ala Ala Leu Lys His
275 280 285
Ala Gly Leu Leu
290